

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/520,258
Source: PJ/10
Date Processed by STIC: 1/13/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 01/13/2005

PATENT APPLICATION: US/10/520,258

TIME: 17:15:06

Input Set : A:\20050-00003.ST25.txt

Output Set: N:\CRF4\01132005\J520258.raw

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1 <110> APPLICANT: NEXGEN BIOTECHNOLOGIES, INC.
2     SHONG, Min-Ho
3     LEE, Sun
4     YOO, Jae-Geun
5     JIN, Seok-Min
7 <120> TITLE OF INVENTION: Production of Transformed Plants Expressing Thyroid
Stimulating
8     Hormone Receptor
10 <130> FILE REFERENCE: 20050-00003
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/520,258
C--> 12 <141> CURRENT FILING DATE: 2005-01-04
12 <150> PRIOR APPLICATION NUMBER: KR2002-38064
13 <151> PRIOR FILING DATE: 2002-07-02
15 <150> PRIOR APPLICATION NUMBER: PCT/KR2003/001308
16 <151> PRIOR FILING DATE: 2003-07-02
18 <160> NUMBER OF SEQ ID NOS: 2
20 <170> SOFTWARE: KopatentIn 1.71
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 2292
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(2289)
31 <400> SEQUENCE: 1
32 atg agg ccg gcg gac ttg ctg cag ctg gtg ctg ctg ctc gac ctg ccc      48
33 Met Arg Pro Ala Asp Leu Leu Gln Leu Val Leu Leu Leu Asp Leu Pro
34 1 5 10 15
36 agg gac ctg gcc gga atg ggg tgt tgc tct cca ccc tgc gag tgc cat      96
37 Arg Asp Leu Gly Gly Met Gly Cys Ser Ser Pro Pro Cys Glu Cys His
38 20 25 30
40 cag gag gag gac ttc aga gtc acc tgc aag gat att caa cgc atc ccc      144
41 Gln Glu Glu Asp Phe Arg Val Thr Cys Lys Asp Ile Gln Arg Ile Pro
42 35 40 45
44 agc tta ccg ccc agt acg cag act ctg aag ctt att gag act cac ctg      192
45 Ser Leu Pro Pro Ser Thr Gln Thr Leu Lys Leu Ile Glu Thr His Leu
46 50 55 60
48 aga act att cca agt cat gca ttt tct aat ctg ccc aat att tcc aga      240
49 Arg Thr Ile Pro Ser His Ala Phe Ser Asn Leu Pro Asn Ile Ser Arg
50 65 70 75 80
52 atc tac gta tct ata gat gtg act ctg cag cag ctg gaa tca cac tcc      288
53 Ile Tyr Val Ser Ile Asp Val Thr Leu Gln Leu Glu Ser His Ser
54 85 90 95
56 ttc tac aat ttg agt aaa gtg act cac ata gaa att cgg aat acc agg      336

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57	Phe	Tyr	Asn	Leu	Ser	Lys	Val	Thr	His	Ile	Glu	Ile	Arg	Asn	Thr	Arg	
58				100					105					110			
60	aac	tta	act	tac	ata	gac	cct	gat	gcc	ctc	aaa	gag	ctc	ccc	ctc	cta	384
61	Asn	Leu	Thr	Tyr	Ile	Asp	Pro	Asp	Ala	Leu	Lys	Glu	Leu	Pro	Leu	Leu	
62			115					120					125				
64	aag	tcc	ttg	gca	ttt	tca	aac	act	gga	ctt	aaa	atg	ttc	cct	gac	ctg	432
65	Lys	Ser	Leu	Ala	Phe	Ser	Asn	Thr	Gly	Leu	Lys	Met	Phe	Pro	Asp	Leu	
66		130					135				140						
68	acc	aaa	gtt	tat	tcc	act	gat	ata	ttc	ttt	ata	ctt	gaa	att	aca	gac	480
69	Thr	Lys	Val	Tyr	Ser	Thr	Asp	Ile	Phe	Phe	Ile	Leu	Glu	Ile	Thr	Asp	
70	145					150				155					160		
72	aac	cct	tac	atg	acg	tca	atc	cct	gtg	aat	gct	ttt	cag	gga	cta	tgc	528
73	Asn	Pro	Tyr	Met	Thr	Ser	Ile	Pro	Val	Asn	Ala	Phe	Gln	Gly	Leu	Cys	
74				165					170				175				
76	aat	gaa	acc	ttg	aca	ctg	aag	ctg	tac	aac	aat	ggc	ttt	act	tca	gtc	576
77	Asn	Glu	Thr	Leu	Thr	Leu	Lys	Leu	Tyr	Asn	Asn	Gly	Phe	Thr	Ser	Val	
78			180					185					190				
80	caa	gga	tat	gat	ttc	ttt	ggg	aca	aag	ctg	gat	gct	gtt	tac	cta	aac	624
81	Gln	Gly	Tyr	Asp	Phe	Phe	Gly	Thr	Lys	Leu	Asp	Ala	Val	Tyr	Leu	Asn	
82		195					200				205						
84	aag	aat	aaa	tac	ctg	aca	gtt	att	gac	aaa	gat	gca	ttt	gga	gga	gta	672
85	Lys	Asn	Lys	Tyr	Leu	Thr	Val	Ile	Asp	Lys	Asp	Ala	Phe	Gly	Gly	Val	
86		210				215				220							
88	tac	agt	gga	cca	agc	ttg	ctg	gac	gtg	tct	caa	acc	agt	gtc	act	gcc	720
89	Tyr	Ser	Gly	Pro	Ser	Leu	Leu	Asp	Val	Ser	Gln	Thr	Ser	Val	Thr	Ala	
90	225				230				235				240				
92	ctt	cca	tcc	aaa	ggc	ctg	gag	cac	ctg	aag	gaa	ctg	ata	gca	aga	aac	768
93	Leu	Pro	Ser	Lys	Gly	Leu	Glu	His	Leu	Lys	Glu	Leu	Ile	Ala	Arg	Asn	
94			245					250				255					
96	agc	tgg	act	ctt	aag	aaa	ctt	gca	ctt	tcc	ttg	agt	ttc	ctt	cac	ctc	816
97	Ser	Trp	Thr	Leu	Lys	Lys	Leu	Ala	Leu	Ser	Leu	Ser	Phe	Leu	His	Leu	
98		260					265				270						
100	aca	cgg	gct	gac	ctt	tct	tac	cca	agc	cac	tgc	tgt	gct	ttt	aag	aat	864
101	Thr	Arg	Ala	Asp	Leu	Ser	Tyr	Pro	Ser	His	Cys	Cys	Ala	Phe	Lys	Asn	
102		275					280				285						
104	cag	aag	aaa	atc	aga	gga	atc	ctt	gag	tcc	ttg	atg	tgt	aat	gag	agc	912
105	Gln	Lys	Lys	Ile	Arg	Gly	Ile	Leu	Glu	Ser	Leu	Met	Cys	Asn	Glu	Ser	
106		290				295			300								
108	agt	atc	gag	acg	ttg	cgc	cag	aga	aaa	tct	gtg	aat	gcc	ttg	aat	agc	960
109	Ser	Ile	Glu	Thr	Leu	Arg	Gln	Arg	Lys	Ser	Val	Asn	Ala	Leu	Asn	Ser	
110	305				310				315				320				
112	ccc	ctc	cac	cag	gaa	tat	gaa	gag	aat	ctg	ggt	gac	agc	att	gtt	ggg	1008
113	Pro	Leu	His	Gln	Glu	Tyr	Glu	Glu	Asn	Leu	Gly	Asp	Ser	Ile	Val	Gly	
114			325					330				335					
116	tac	aag	gaa	aag	tcc	aag	ttc	cag	gat	act	cat	aac	aac	gct	cat	tat	1056
117	Tyr	Lys	Glu	Lys	Ser	Lys	Phe	Gln	Asp	Thr	His	Asn	Asn	Ala	His	Tyr	
118		340					345				350						
120	tac	gtc	ttc	ttt	gaa	gaa	caa	gag	gat	gag	atc	att	ggt	ttt	ggc	cag	1104
121	Tyr	Val	Phe	Phe	Glu	Glu	Gln	Glu	Asp	Glu	Ile	Ile	Gly	Phe	Gly	Gln	

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122	355	360	365	
124	gag ctc aaa aac ccc cag gaa gag act cta caa gct ttt gac agc cat	1152		
125	Glu Leu Lys Asn Pro Gln Glu Glu Thr Leu Gln Ala Phe Asp Ser His			
126	370 375 380			
128	tat gac tac acc ata tgt ggg gac agt gaa gac atg gtg tgt acc ccc	1200		
129	Tyr Asp Tyr Thr Ile Cys Gly Asp Ser Glu Asp Met Val Cys Thr Pro			
130	385 390 395 400			
132	aag tcc gat gag ttc aac ccg tgt gaa gac ata atg ggc tac aag ttc	1248		
133	Lys Ser Asp Glu Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Lys Phe			
134	405 410 415			
136	ctg aga att gtg gtg tgg ttc gtt agt ctg ctg gct ctc ctg ggc aat	1296		
137	Leu Arg Ile Val Val Trp Phe Val Ser Leu Leu Ala Leu Leu Gly Asn			
138	420 425 430			
140	gtc ttt gtc ctg ctt att ctc ctc acc agc cac tac aaa ctg aac gtc	1344		
141	Val Phe Val Leu Leu Ile Leu Leu Thr Ser His Tyr Lys Leu Asn Val			
142	435 440 445			
144	ccc cgc ttt ctc atg tgc aac ctg gcc ttt gcg gat ttc tgc atg ggg	1392		
145	Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp Phe Cys Met Gly			
146	450 455 460			
148	atg tac ctg ctc ctc atc gcc tct gta gac ctc tac act cac tct gag	1440		
149	Met Tyr Leu Leu Leu Ile Ala Ser Val Asp Leu Tyr Thr His Ser Glu			
150	465 470 475 480			
152	tac tac aac cat gcc atc gac tgg cag aca ggc cct ggg tgc aac acg	1488		
153	Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Pro Gly Cys Asn Thr			
154	485 490 495			
156	gct ggt ttc ttc act gtc ttt gca agc gag tta tcg gtg tat acg ctg	1536		
157	Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu			
158	500 505 510			
160	acg gtc atc acc ctg gag cgc tgg tat gcc atc acc ttc gcc atg gcc	1584		
161	Thr Val Ile Thr Leu Glu Arg Trp Tyr Ala Ile Thr Phe Ala Met Ala			
162	515 520 525			
164	ctg gac cgg aag atc cgc ctc agg cac gca tgt gcc atc atg gtt ggg	1632		
165	Leu Asp Arg Lys Ile Arg Leu Arg His Ala Cys Ala Ile Met Val Gly			
166	530 535 540			
168	ggc tgg gtt tgc tgc ttc ctt ctc gcc ctg ctt cct ttg gtg gga ata	1680		
169	Gly Trp Val Cys Cys Phe Leu Leu Ala Leu Leu Pro Leu Val Gly Ile			
170	545 550 555 560			
172	agt agc tat gcc aaa gtc agt atc tgc ctg ccc atg gac acc gag acc	1728		
173	Ser Ser Tyr Ala Lys Val Ser Ile Cys Leu Pro Met Asp Thr Glu Thr			
174	565 570 575			
176	cct ctt gct ctg gca tat att gtt ttt gtt ctg acg ctc aac ata gtt	1776		
177	Pro Leu Ala Leu Ala Tyr Ile Val Phe Val Leu Thr Leu Asn Ile Val			
178	580 585 590			
180	gcc ttc gtc atc gtc tgc tgc tgt tat gtg aag atc tac atc aca gtc	1824		
181	Ala Phe Val Ile Val Cys Cys Cys Tyr Val Lys Ile Tyr Ile Thr Val			
182	595 600 605			
184	cga aat ccg cac aac cca ggg gac aaa gat acc aaa att gcc aag agg	1872		
185	Arg Asn Pro His Asn Pro Gly Asp Lys Asp Thr Lys Ile Ala Lys Arg			
186	610 615 620			

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188 atg gct gtg ttg atc ttc acc gac ttc acg tgc atg gcc cca atc tca      1920
189 Met Ala Val Leu Ile Phe Thr Asp Phe Thr Cys Met Ala Pro Ile Ser
190 625                      630                      635                      640
192 ttc tat gct gtg tca gca att ctg aac aag cct ctc atc act gtt agc      1968
193 Phe Tyr Ala Val Ser Ala Ile Leu Asn Lys Pro Leu Ile Thr Val Ser
194                      645                      650                      655
196 aac tcc aaa atc ttg ctg gta ctc ttc tat cca att aac tcc tgt gcc      2016
197 Asn Ser Lys Ile Leu Leu Val Leu Phe Tyr Pro Ile Asn Ser Cys Ala
198                      660                      665                      670
200 aat cca ttc ctc tat gct att ttc acc aag gcc ttc cag agg gat gtg      2064
201 Asn Pro Phe Leu Tyr Ala Ile Phe Thr Lys Ala Phe Gln Arg Asp Val
202                      675                      680                      685
204 ttc atc cta ctc agc aag ttt ggc atc tgt aaa cgc cag gct cag gca      2112
205 Phe Ile Leu Leu Ser Lys Phe Gly Ile Cys Lys Arg Gln Ala Gln Ala
206                      690                      695                      700
208 tac cgg ggg cag agg gtt cct cca aag aac agc act gat att cag gtt      2160
209 Tyr Arg Gly Gln Arg Val Pro Pro Lys Asn Ser Thr Asp Ile Gln Val
210 705                      710                      715                      720
212 caa aag gtt acc cac gac atg agg cag ggt ctc cac aac atg gaa gat      2208
213 Gln Lys Val Thr His Asp Met Arg Gln Gly Leu His Asn Met Glu Asp
214                      725                      730                      735
216 gtc tat gaa ctg att gaa aac tcc cat cta acc cca aag aag caa ggc      2256
217 Val Tyr Glu Leu Ile Glu Asn Ser His Leu Thr Pro Lys Lys Gln Gly
218                      740                      745                      750
220 caa atc tca gaa gag tat atg caa acg gtt ttg                      t aa      2292
221 Gln Ile Ser Glu Glu Tyr Met Gln Thr Val Leu
222                      755                      760
225 <210> SEQ ID NO: 2
226 <211> LENGTH: 763
227 <212> TYPE: PRT
228 <213> ORGANISM: Homo sapiens
230 <400> SEQUENCE: 2
231 Met Arg Pro Ala Asp Leu Leu Gln Leu Val Leu Leu Leu Asp Leu Pro
232 1                      5                      10                      15
234 Arg Asp Leu Gly Gly Met Gly Cys Ser Ser Pro Pro Cys Glu Cys His
235                      20                      25                      30
237 Gln Glu Glu Asp Phe Arg Val Thr Cys Lys Asp Ile Gln Arg Ile Pro
238                      35                      40                      45
240 Ser Leu Pro Pro Ser Thr Gln Thr Leu Lys Leu Ile Glu Thr His Leu
241                      50                      55                      60
243 Arg Thr Ile Pro Ser His Ala Phe Ser Asn Leu Pro Asn Ile Ser Arg
244 65                      70                      75                      80
246 Ile Tyr Val Ser Ile Asp Val Thr Leu Gln Gln Leu Glu Ser His Ser
247                      85                      90                      95
249 Phe Tyr Asn Leu Ser Lys Val Thr His Ile Glu Ile Arg Asn Thr Arg
250                      100                     105                     110
252 Asn Leu Thr Tyr Ile Asp Pro Asp Ala Leu Lys Glu Leu Pro Leu Leu
253                      115                     120                     125
255 Lys Ser Leu Ala Phe Ser Asn Thr Gly Leu Lys Met Phe Pro Asp Leu

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256      130      135      140
258 Thr Lys Val Tyr Ser Thr Asp Ile Phe Phe Ile Leu Glu Ile Thr Asp
259 145      150      155      160
261 Asn Pro Tyr Met Thr Ser Ile Pro Val Asn Ala Phe Gln Gly Leu Cys
262      165      170      175
264 Asn Glu Thr Leu Thr Leu Lys Leu Tyr Asn Asn Gly Phe Thr Ser Val
265      180      185      190
267 Gln Gly Tyr Asp Phe Phe Gly Thr Lys Leu Asp Ala Val Tyr Leu Asn
268      195      200      205
270 Lys Asn Lys Tyr Leu Thr Val Ile Asp Lys Asp Ala Phe Gly Gly Val
271      210      215      220
273 Tyr Ser Gly Pro Ser Leu Leu Asp Val Ser Gln Thr Ser Val Thr Ala
274 225      230      235      240
276 Leu Pro Ser Lys Gly Leu Glu His Leu Lys Glu Leu Ile Ala Arg Asn
277      245      250      255
279 Ser Trp Thr Leu Lys Lys Leu Ala Leu Ser Leu Ser Phe Leu His Leu
280      260      265      270
282 Thr Arg Ala Asp Leu Ser Tyr Pro Ser His Cys Cys Ala Phe Lys Asn
283      275      280      285
285 Gln Lys Lys Ile Arg Gly Ile Leu Glu Ser Leu Met Cys Asn Glu Ser
286      290      295      300
288 Ser Ile Glu Thr Leu Arg Gln Arg Lys Ser Val Asn Ala Leu Asn Ser
289 305      310      315      320
291 Pro Leu His Gln Glu Tyr Glu Glu Asn Leu Gly Asp Ser Ile Val Gly
292      325      330      335
294 Tyr Lys Glu Lys Ser Lys Phe Gln Asp Thr His Asn Asn Ala His Tyr
295      340      345      350
297 Tyr Val Phe Phe Glu Glu Gln Glu Asp Glu Ile Ile Gly Phe Gly Gln
298      355      360      365
300 Glu Leu Lys Asn Pro Gln Glu Glu Thr Leu Gln Ala Phe Asp Ser His
301      370      375      380
303 Tyr Asp Tyr Thr Ile Cys Gly Asp Ser Glu Asp Met Val Cys Thr Pro
304 385      390      395      400
306 Lys Ser Asp Glu Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Lys Phe
307      405      410      415
309 Leu Arg Ile Val Val Trp Phe Val Ser Leu Leu Ala Leu Leu Gly Asn
310      420      425      430
312 Val Phe Val Leu Leu Ile Leu Leu Thr Ser His Tyr Lys Leu Asn Val
313      435      440      445
315 Pro Arg Phe Leu Met Cys Asn Leu Ala Phe Ala Asp Phe Cys Met Gly
316      450      455      460
318 Met Tyr Leu Leu Leu Ile Ala Ser Val Asp Leu Tyr Thr His Ser Glu
319 465      470      475      480
321 Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Pro Gly Cys Asn Thr
322      485      490      495
324 Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu
325      500      505      510
327 Thr Val Ile Thr Leu Glu Arg Trp Tyr Ala Ile Thr Phe Ala Met Ala
328      515      520      525

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VERIFICATION SUMMARY

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Input Set : A:\20050-00003.ST25.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date